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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/865,090	05/24/2001	Harold R. Garner	UTSD:0668	2902

23379 7590 02/06/2004

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EXAMINER

WONG, LESLIE

ART UNIT	PAPER NUMBER
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2177

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DATE MAILED: 02/06/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

## Office Action Summary

Application No.

09/865,090

Applicant(s)

GARNER ET AL.

Examiner

Leslie Wong

Art Unit

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 09 December 2003.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 1-24 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-24 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. §§ 119 and 120

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- \* See the attached detailed Office action for a list of the certified copies not received.
- 13) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application) since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.
- a) ☐ The translation of the foreign language provisional application has been received.
- 14) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121 since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

### Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) \_\_\_\_\_
- 4) ☐ Interview Summary (PTO-413) Paper No(s). \_\_\_\_\_
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other:

## DETAILED ACTION

### *Response to Amendment*

1. Receipt of Applicants' Amendment, filed 09 December 2003, is acknowledged. The amendment to the Specification has overcome the rejection indicated in the Office Action dated 19 October 2003.

### *Claim Rejections - 35 USC § 103*

2. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

3. Claims 1, 3, 6, and 8-24 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al. "Wolffe"** (US 2002/0081603 A1) and in view of **Hennig et al. "Hennig"** (A data-analysis pipeline for large-scale gene expression analysis).

Regarding claims 1, 13, and 17, **Wolffe** teach computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding annotations, the system comprising:

a). a search function which searches the annotations of the dataset according to a user defined criterion and outputs a first subset of the dataset restricted by the criterion (§s 0397, 0398).

c). a selection function which applies to the second subset a user-defined selection parameter and outputs a third subset restricted relative to the second subset by the parameter (§s 358, 386) .

d). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the third subset (§s 350, 391, 392).

b). **Wolffe** does not explicitly teach a redundancy reducing function which compares the first subset with a first database correlating the sequence identifiers of the first subset with syngeneic biopolymers and outputs a second subset of the dataset having **reduced unique**, natural complex biopolymer **redundancy** relative to the first subset.

**Hennig**, however, teaches a redundancy reducing function which compares the first subset with a first database correlating the sequence identifiers of the first subset

with syngeneic biopolymers and outputs a second subset of the dataset having reduced unique, natural complex biopolymer redundancy relative to the first subset (Section 2.5.1 Cleaning of raw sequence data; Section 1. Introduction, lines 1-4, and Section 2.2. Image Analysis, last paragraph).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Hennig's** teaching would have allowed **Wolffe's** to clean, remove duplicates, and perform quality checks to the raw sequence in preparation for the sequence comparative analysis as indicated in Section 1 – Introduction, lines 1-11 and Section 2.2. Image Analysis, last paragraph.

Regarding claims 3 and 6, **Wolffe** further teach wherein the criterion is one of a plurality of user-defined criteria, and the search function searches the annotations of the dataset according to the criteria and outputs a first subset of the dataset restricted by the criteria (¶s 0397, 0398).

Regarding claims 8 and 11, **Hennig** further teach wherein the database is one of a plurality of databases correlating the sequence identifiers of the first subset with syngeneic biopolymers, and the redundancy reducing function compares the first subset with the databases and outputs the second subset of the dataset (Section 2.5.1 Cleaning of raw sequence data; Section 1. Introduction, lines 1-4, and Section 2.2. Image Analysis, last paragraph).

Regarding claims 9 and 16, **Wolffe** further teach wherein the parameter is selected from the group consisting of source (i.e., Genbank), species, author, and pathway (§s 002, 99, 234).

Regarding claim 10, **Wolffe** further teach wherein the parameter is one of a plurality of user-defined selection parameters, and the selection function applies to the second subset the parameters and outputs the third subset restricted relative to the second subset by the parameters (§s 0397, 0398).

Regarding claim 12, **Wolffe** further teach comprising an expansion function which searches a second database for synonyms of the sequence identifiers of the first, second or third subset (§s 0132, 0133).

Regarding claim 19, **Wolffe** further teach wherein the second annotations comprise data attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset, said data selected from the group consisting of: gene expression data, sequencing data, genotype data, polymorphism data and clinical data (§s 0006, 0031, 0083, 299, and 0322).

Regarding claims 14, 15, 18, 20, 21, 22, and 23, **Wolffe** further teach steps of:

b). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset (¶s 350, 391, 392).

c). a third computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding first annotations, the third system comprising:

1). an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which link, the second annotations to the corresponding sequence identifiers of the subset (¶s 0038-0042; 344); and

2). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations (¶s 350, 391, 392).

a). **Wolffe** does not explicitly teach a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngeneic biopolymers and creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer **redundancy** relative to the sum.

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**Hennig**, however, teaches a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngeneic biopolymers and creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer **redundancy** relative to the sum (Section 2.5.1 Cleaning of raw sequence data; Section 1. Introduction, lines 1-4, and Section 2.2. Image Analysis, last paragraph).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Hennig's** teaching would have allowed **Wolffe's** to clean, remove duplicates, and perform quality checks to the raw sequence in preparation for the sequence comparative analysis as indicated in Section 1 – Introduction, lines 1-11 and Section 2.2. Image Analysis, last paragraph.

Regarding claim 24, **Wolffe** further teach wherein the system is ARROGANT (¶ 0012). The cited portion facilitates identification, analysis, and comparison of collections of genes and clones. Therefore, it is equivalent to the ARROGANT system.

4. Claims 2 and 4 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al. "Wolffe"** (US 2002/0081603 A1) and in view of **Hennig et al. "Hennig"** (A data-analysis pipeline for large-scale gene expression analysis) as applied to claims 1, 3, 6, and 8-24 above, and further in view of **Lincoln et al. "Lincoln"** (U.S. Patent 6,303,297).



Regarding claim 2, **Wolffe** and **Hennig** do not explicitly teach wherein the criterion is selected from the group consisting of a keyword and a concept.

**Lincoln**, however, teaches wherein the criterion is selected from the group consisting of a keyword and a concept (col. 20, lines 38-50).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Lincoln's** teaching would have allowed **Wolffe** and **Hennig's** the ability to access genetic information to perform comparative analysis in a more effective manner as users can enter a search concept via keywords as disclosed in col. 20, lines 38-44.

Regarding claim 4, **Wolffe** further teach wherein the criterion is one of a plurality of user-defined criteria, and the search function searches the annotations of the dataset according to the criteria and outputs a first subset of the dataset restricted by the criteria (§§s 0397, 0398).

**Wolffe** and **Hennig** do not explicitly teach wherein the criteria include multiple keywords.

**Lincoln**, however, teaches wherein the criteria include multiple keywords (col. 20, lines 42-44).

5. Claim 5 is rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al.** "**Wolffe**" (US 2002/0081603 A1) and in view of **Hennig et al.** "**Hennig**" (A data-

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analysis pipeline for large-scale gene expression analysis) as applied to claims 1, 3, 6, and 8-24 above, and further in view of **Chin et al.** (U.S. Patent 6,470,277).

Regarding claim 5, **Wolffe** further teach wherein the dataset is selected from GenBank (§ 0348).

**Wolffe** and **Hennig** do not explicitly do not explicitly teach wherein the dataset is selected from the group consisting GenBank, Medline, and KEGG.

**Chin et al.**, however, teach wherein the dataset is selected from the group consisting Medline and KEGG (col. 11, lines 29-46; col. 18, lines 54-59).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Chin's** teaching would have allowed **Wolffe** and **Hennig's** to include Medline and KEGG for sequence searching because these databases contain functional information related to known genes and would be helpful for researchers to be able to access the mentioned databases.

6. Claim 7 is rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al.** "**Wolffe**" (US 2002/0081603 A1) and in view of **Hennig et al.** "**Hennig**" (A data-analysis pipeline for large-scale gene expression analysis) as applied to claims 1, 3, 6, and 8-24 above, and further in view of **MacLeod et al.** (U.S. Patent 6,221,600 B1).

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Regarding claim 7, **Wolffe** does not explicitly teach wherein the database is selected from the group consisting of UniGene and LocusLink.

**Hennig** teaches wherein the database is selected from the group consisting of Genbank, Swissprot+Tremble, Unigene, dbEst, GeneCards, and a lab-internal EST database (Section 2.5.2 Data base mining and handling of results, first paragraph).

**Wolffe** and **Hennig** do not explicitly teach wherein the database is selected from the group consisting of LocusLink.

**MacLeod et al.**, however, teach wherein the database is selected from the group consisting of UniGene and LocusLink (col. 13, lines 43-58).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Chin's** teaching would have allowed **Wolffe** and **Hennig's** users to have access to UniGene and LocusLink to search and create collections of sequences as this would provide various of sources for users to search, extract, and manipulate the information.

### ***Conclusion***

7. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

**Spier et al.** (US 2003/0082572 A1).

**Lincoln et al.** (U.S. Patent 6,553,317 B1).

**Wang et al.** (Combinatorial Pattern Discovery for Scientific Data: Some Preliminary Results).

**King et al.** (Genome Scale Prediction of Protein Functional Class from Sequence using Data Mining).

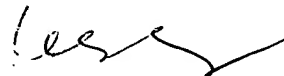
***Response to Argument***

8. Applicant's arguments with respect to claims 1-24 have been considered but are moot in view of the new ground(s) of rejection.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Leslie Wong whose telephone number is (703) 305-3018. The examiner can normally be reached on Monday to Friday 9:30am - 6:30 pm.


If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John E Breene can be reached on (703) 305-9790. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 305-3900.



Leslie Wong  
Patent Examiner  
Art Unit 2177

Lw  
28 January 2004



JEAN R. HOMERE  
PRIMARY EXAMINER